

Amendments to the Specification

At page 1, after the Title, please amend the paragraph as follows:

This application is a continuation of U.S. Application No. 09/561,779, filed May 1, 2000, now abandoned; which is a continuation of International Application No. PCT/US98/22965, having an international filing date of 30 October 1998 and published under PCT Article 21(2) in English on 14 May 1999, said International Application claiming the benefit under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 60/063,571, filed October 30, 1997; all of which are incorporated in their entirety by reference herein.

At page 11, lines 4-6, please amend the paragraph as follows:

{We could disclose the various expression vectors which were generated to express SVPH1-26 polypeptides. We should include the preferred method of expressing SVPH1-26 polypeptides known to the inventor.}

Please amend the paragraph bridging pages 3 and 4 as follows:

When a peptide fingerprint of an unknown protein is obtained, this can be compared to a database of known proteins to assist in the identification of the unknown protein (W.J. Henzel et al., *Proc. Natl. Acad. Sci. USA* 90:5011-5015, 1993; B. Thiede et al., *Electrophoresis* 1996, 17:588-599, 1996). A variety of computer software programs are accessible via the Internet to the skilled artisan for the facilitation of such comparisons, such as MultiIdent (Internet site: ~~www~~www.expasy.ch/sprot/multiident.html), PeptideSearch (Internet site: ~~www~~[mann.embl-heidelberg.de...deSearch/FR_PeptideSearchForm.html](http://mann.embl-heidelberg.de/deSearch/FR_PeptideSearchForm.html)), and ProFound (Internet site: ~~www~~[www.chait-sgi.rockefeller.edu/cgi-bin/prot-id-frag.html](http://chait-sgi.rockefeller.edu/cgi-bin/prot-id-frag.html)). These programs allow the user to specify the cleavage agent and the molecular weights of the fragmented peptides within a designated tolerance. The programs compare these molecular weights to protein databases to assist in the elucidation of the identity of the sample protein. Accurate information concerning the number of fragmented peptides and the precise molecular weight of those peptides is required for accurate identification. Therefore, increasing the accuracy in the determination of the number of fragmented peptides and the precise molecular weight of those peptides should result in enhanced success in the identification of unknown proteins.